

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 7, 2001, 00:17:07 ; Search time 54.85 Seconds

(without alignments)
1617.619 Million cell updates/sec

Title: US-09-494-297-2

Sequence: 1 MKTRFPKNTLTQRYLS.....IAGISLGITGHTIRIKHD 757

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_15:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_unclassified:*

13: sp_vertebrate:*

14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1965.5	49.8	742	2	092B47
2	633.5	16.1	659	2	054953
3	611	15.5	685	2	033709
4	603	15.3	688	2	001924
5	523	13.3	580	2	047942
6	272.5	6.9	106	2	033715
7	262.5	6.7	104	2	033714
8	241.5	6.1	108	2	033711
9	222.5	5.6	116	2	033712
10	211.5	5.4	92	2	033718
11	210.5	5.4	103	2	033719
12	210.5	5.3	102	2	033716
13	209.5	5.3	102	2	033716
14	205.5	5.2	93	2	033720
15	204.5	5.1	102	2	033710
16	202.5	4.7	84	2	033717
17	185	4.6	597	2	P72A16
18	180	4.5	898	2	085081
19	178				085081 moraxella c

20	176	4.5	905	2	085088
21	164	4.2	1039	2	P72534
22	159	4.0	1243	2	048588
23	158.5	4.0	3269	2	09RGN5
24	157.5	4.0	5005	2	09P25
25	152	3.9	2516	2	09RM43
26	151	3.8	2367	2	046034
27	150	3.8	1161	2	09X3M7
28	149	3.8	1315	2	086488
29	148.5	3.8	1883	2	09PPT2
30	147	3.7	1563	2	09VAF5
31	145	3.7	1036	2	086999
32	144.5	3.7	1092	2	070022
33	143.5	3.6	1433	2	045616
34	143.5	3.6	1915	2	09RPL0
35	142.5	3.6	627	2	030643
36	142.5	3.6	1032	5	061207
37	142	3.6	931	2	09K113
38	139.5	3.5	888	2	09P009
39	139.5	3.5	1167	2	09ZLG7
40	138.5	3.5	625	2	030704
41	138.5	3.5	2484	5	09U347
42	138.5	3.5	2607	5	023187
43	138	3.5	894	2	085085
44	137	3.5	687	5	09W3D6
45	136	3.4	922	13	P79883

ALIGNMENTS

RESULT 1

ID 092B47 PRELIMINARY; PRT; 742 AA.

AC 092B47;

DT 01-MAY-1999 (T-EMBLrel. 10, Created)

DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)

DT 01-MAY-2000 (T-EMBLrel. 13, Last annotation update)

DE CPA.

GN Streptococcus pyogenes.

OS Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;

OC Streptococcus.

NCBI_TaxID=1314;

ON [1]

RP SEQUENCE FROM N.A.

RC STRAIN-CS101;

RA Podbielski A., Woischnik M., Leonard B.A.B., Schmidt K.H.,

RT "Characterization of nra, a global negative regulator gene in group A

RL Mol. Microbiol. 31:0-0(1999).

DR EMBL: U49397; AAC97148.1; .

SQ SEQUENCE 742 AA; 83682 MW; 97A1FF44BAECB944 CRC64;

Query Match 49.8%; Score 1965.5; DB 2; Length 742;

Best Local Similarity 54.4%; Pred. No. 2.3e-108;

Matches 401; Conservative 116; Mismatches 195; Indels 25; Gaps 13;

QY 20 SKSKR--FTVTLVGFLMFAVLTVSMVGAKYFGLVESTPNAINDSSSEYRWYGES 77

DB 11 SANMKRQTTIGLKVFLTFVALIGVFSIRAFGEQSPN--ROSSIODYPWGYS 68

QY 78 YVRGHPRYKQFRAVHADRNVLEGSRSYQVCFNLKKAFLPGSDSVYKWKYKKHGDISTKF 137

DB 69 YPKGIDYSPKTYHNHKNVLEBSKDYQATCFNLTKHFPKSSVSNSQWYKKLEGTFNPF 128

QY 138 EDYAMSPRITDELNOKIRAVMYNGHPQANGIMEGLEPLNARVYQEAVMYVSDNAPIS 197

DB 129 IRLADKRIEDGQLQNLILILVNGVYNNRNGIMKIGIDPLNALIVQNALW--YTDNQI- 186

QY 198 NPDSFKRESSESNVSTQSLMKRQALKLIDPNLATKMKQVPDFQLSIFSESDKGD 257

||||| : : : || :||| :||| :| :| :||| :|

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Db 187 NPDESEKTEARSNGINDOQGLMRKALKELIDENLGSKYSNKTSPSGRLNVFESH----- 242
QY 258 YNGGYONLISGGLVPTKPPPGDPPMPNPQPTTSVILIRKATAGDSKYLEGATLOLTD 317
Db 243 --KPFONLISAERYVDPDPKPGEE--PPAKTEKTSVILIRKAEED--SKLEGATLKLSQI 297
QY 318 NVMSFOARVSSNDIGERIELSDGYTLTLELNSPAGYSIAEPTFKYEAQKVTYI-IDGK 376
Db 298 ESGGFQEKDFQSNLSGTLVLPNGTYTLTETSSPDGKIKIEPIKFRKNKVFIVQKDS 357
QY 377 QINPNKEIPEYPSVEAYNDPEEFSVLT-TQNYAKFYAAKNKNGSSOVVYCFNADLKSP 435
Db 358 QVENPNKEVAPYPSVEAYNPFMDPEVLSGFTPYGKFYATANKDKSSOVVYCFNADLHSP 417
QY 436 DSDDGCKTMTPTT-GEVYTHIAGRLFKYVKKPRDTPDPTFLKIKKIVIEKGYEK 494
Db 418 DSDSGETTPDPTSTYMEVYTHIAGSLDFKVALPRDTPDEDFLKIKKIVIEKGYKKG 477
QY 495 QAIEYSGLTETQLRAATQALAIYFTDSAEIDKDKL-----KDYHGFCDMDNSTLAVAKLV 550
Db 478 DS--YNGLETQGRANQALAIYFTDSADLTKLTYNNGSGYHGFESMDKTLAVTKELI 535
QY 551 EYADSNPQDLDLDFPIPNKKYOSLIGTQHPEDLVIIKMDKK-EVYPTVHTLTLR 609
Db 536 TYAONGSAPQDLDLDFEVPNNKSDOSLIGTECHPDLDLVYIRMEDKKOEYIPTYHSLTVK 595
QY 610 KYTVGLAGDRTDFHFEIELKNNKOEELISQTVKTDKTNLEFKDGKATINLKHGESLTLOG 669
Db 596 KTYVGLGDKTKGFQFLELAKDTGQPIVNTLKTNNODLAKDKGYSFNLKHGDTLIEG 655
QY 670 LPEGYSTLVKETDSEGYKRVNSQEVANATVSKTGITSDETLAFENKKEPVPTGVQDKI 729
Db 656 LPTGYSTLKEAKAKQDIYVVDKNKVSQEQSGVDITEDKRVTFENKRDLVPTGLTTDG 715
QY 730 NGYLAIVINAGISLGT 746
Db 716 AYLMLLLVPIGLVW 732

RESULT 2
ID 054953 PRELIMINARY; PRT; 659 AA.
AC 054953;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, last annotation update)
DE PROTEIN F.
GN PROTEIN F.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JRS75;
RC MEDLINE=95020565; PubMed=7934855;
RA Sela S., Aviv A., Burshten I., Tovl A., Caparon M.G., Hanaki E.;
RT Protein F: an adhesin of Streptococcus pyogenes binds fibrinectin via
RT two distinct domains";
RL Mol. Microbiol. 10:1049-1055(1993).
DR EMBL; L10919; AAA26964.1; -.
DR INTERPRO; IPR001899; -.
DR PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOMN.1.
SQ SEQUENCE 659 AA; 73628 MW; DQCEB91D159726BD CRC64;

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Query Match 16.1%; Score 633.5; DB 2: Length 659;
 Best Local Similarity 26.1%; Pred. No. 1.4e-29;
 Matches 203; Conservative 128; Mismatches 237; Indels 211; Gaps 30;

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QY 20 SKRSKREPTVTLVGVFIMFALVTSWVGAKTVFGLVSESTNAINPDSSSTYRYGYESIV 79
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 24 TKRRRFAVTLVGVFIMFALVTSWVGAKTVFGLVSESTNAINPDSSSTYRYGYESIV 81
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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QY 80 RGHPEYKQFRVADHLRVNLEGSRSYOVYCNLKAFFLGSSSVKKMYKHKDISTRKFD 139
Db 82 KEYFGINIKWIRYDHLRVNLENGSRSYOVYCFNIOSTNPQKNSIKMKFKKIEBNGSFVD 141
QY 140 YAMSPRTGDELNOKLRAVYNGHPONANGIMEGLPELNAIRYTOBAVWYYSQNAPISNP 199
Db 142 YAHRTKLGKRELQRLSLILYNAVYPDANGYMKGLEHLNATVTOYAAVWHYSDNSQYGF 200
QY 200 DESFKRESNLSVTSQSLSMRQALQOLDPNATKMPKQVPPDFOLSTFESDKDKDN 259
Db 201 ETLMESEAKKGIKSRQVTLMRALKLIDPNLEAAYVKNIPSGYRLNIFESE-----N 254
QY 260 KGYONLISGGLVPTKPPPGDPPMPNPQPTTSVILIRKVAIGDSKYLEGATL-----OLT 315
Db 255 EAYONLISAERYVDPDPKPGEE--TSEHNKPTPE-----LDGTPLEDPKPH 298
QY 316 GDNVNSFOARVSSNDIGERIELSDGYTLTLELNSPAGYSIAEPTFKYEAQKVTYI-IDG 375
Db 299 DDMLEPTLPVMDL-----GEEV-----PEVPSSELEPALPLMPE-----LDG 337
QY 376 KQIENPKKEIVE-PYSVEAANDPEEFSVLTQNYAKFYAAKNKNGSSOVVYCFNADLKSP 434
Db 338 QEV--PEKPSIDLPTEVPRIE-----FNKRDOSP 364
QY 435 PDSEDEGCKTMTPTTGEVYV-THIAGRLFKYVKKPRDTPDPTFLKIKKIVIEKGYREK 493
Db 365 LAGE-----SGEFTYIEVYGNQ-----QNPVYDIDK-----KLPRTEGF--S 399
QY 494 QAIEYSGLTETQLRAATQALAIYFTDSAEIDKDKLDYHG-----FG 536
Db 400 GNVVETEDTEKEPEVLNGGQ-----SESVFTKDTQMGSGQTPPVETEDTEKEPEVLNG 453
QY 537 DMDNSTLAVAKILVEYAQDS-----NPQDLDLDFPIPNKKYOSLIGTQHPEDLV 589
Db 454 GQSES-----VEFTKDTQMGSGQTPQIETEDTEKEPE----- 486
QY 590 IIRMEDKEEIVPTVHTLTLKTYVGLAGDRTDFHFEIELKNNKQ-ELL-----SQTVKTD 644
Db 487 -VLMGQSESEVEFT-----KDTQMGSGQTP-----QVEIEDTKKEPEVLNGGQSESEVEFT 536
QY 645 KTNLEKDGKATYNLKHGESLVLQGLPEGYSTLVKETDSEBGYKRVNSQEVANATVSKTG 704
Db 537 KDTQMGSGQTPQIETEDTEKEPEVLNGGQSESEVEFT-----KDTQMGSGQSEFA 587
QY 705 ITSDET-----LAFENK-----EPVPT-GVQDKINGYLAIVAGISL 743
Db 588 TVVEDTRPKLVFHFHNNPKEVNEKREKPTKNTPTLPATGDIEVLAVLGLITLVSLI 646

RESULT 3
ID 033709 PRELIMINARY; PRT; 685 AA.
AC 033709;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, last annotation update)
DE FIBRONECTIN/FIBRINOGEN BINDING PROTEIN F.
GN PRF15.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EF1949;
RC MEDLINE=98129085; PubMed=9467904;
RA Katerov V., Andreev A., Schalen C., Totolian A.A.;
RT "Protein F, a fibrinectin-binding protein of Streptococcus pyogenes,
RT also binds human fibrinogen: isolation of the protein and mapping of
RT the binding region.";
RL Microbiology 144:119-126(1998).
DR EMBL; AF009908; AAC38155.1; -.

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QY	193	NAPLSNDESKRESSESNIVSTQSLIMROALQOLIDPNATMKTMPKQVDPDLSIFESE	252
Db	189	NSSLFNDNFETTTAKDLNLRKPELSSLMRAKLKLLIDPKLSSESLKLVVSTFRKLNIFESQ	248
QY	253	DKGDRKYNKYONLLSGGLVPTKPTPGDPPMPNPQOTVSLIRKVAIGDYSKLEGATL	312
Db	249	D-----KLYONLLSAEVRLENPKPGEE--TPHGPKTPEL-----DGTPLPGP--	290
QY	313	QLTDGNVNSFOARPFSSNDIGERLELSDGYTTLTFLNSPAGYSIAETITFKVEAGKYTTI	372
Db	291	QRPNESELTPLPV-----MLDG--QEVPEVSESLPALPLPMBELDQGEVPEV	338
QY	373	-----IDKQI--ENPNKE--IVEPEVSEAYNDEFEESVLTQNYAKFYVA	414
Db	339	PSESLPALPLPMBELDQGEVPEKPSVDLPIEDR-----	373
QY	415	KNNKSSOVVYCFNADLKSPDSESDGKMTPTDFTGEVRY--THIAGRLFKYTVKPRDT	473
Db	374	-----YEFNNKKQSPHAGE-----SGEETETIEVYGNQ-----QNPVDI	407
QY	474	DDDFELKHKKIVIEKGYREKQALIEYSGLTETOLARATOLAIYFTDASLMDKLDYH	533
Db	408	DK-----KLPNETGR--SGNMVETEDTKEPGLMGQ-----SSVFTKDTQTGMS	452
QY	534	GFGDMNDSTLVAKLIVEYADSNP-----QLTDDFEIPNNKKYQSLIGTQWPEDL	587
Db	453	G-----QTTQVGE-----TEDTKEPGLMGQSESEVFTKDTQTGMSQTASQVETEDT	501
QY	588	VDI--IRMDKKEVYRPTHNLRTKTYVGLAGDRKDKDHFELKNNKQELLSTQVTKDKT	646
Db	502	KEPGVLMGQSESEVFT-----KDTQTGMSQOTTP-----QVETEDTKEPGLMGQSE--	550
QY	647	NLEF--KDGKATINKHGESLTLQGLPRGYSVLYVETDSEGGKYKVNQSEYANATVSKTGI	705
Db	551	SVEFTKDTQTGMS--GSESVTIVETDTRPLVAPHFNNEKVEENKEKT-----	598
QY	706	TSDETLAFENKKEPVV--TGYDQKINGTLALIVYA	739
Db	599	-----KNITPLPATGDIENVLAFLGILILS	624
RESULT	5		
Q47942			
AC	Q47942	PRELIMINARY:	PRT: 580 AA.
DT	01-NOV-1996	(TREMBlrel, 01, Created)	
DT	01-NOV-1996	(TREMBlrel, 01, Last sequence update)	
DT	01-MAY-2000	(TREMBlrel, 13, Last annotation update)	
DE	FIBRONECTIN BINDING PROTEIN F.		
GN	GPB.		
OS	Streptococcus sp.		
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;		
OC	Streptococcus.		
OX	NCBI_Taxid=1306;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	SPRAIN-1750.		
RX	MEDLINE=96239026; PubMed=8675316.		
RA	Kline J.B., Xu S., Bisno A.L., Collins C.M.;		
RT	"Identification of a fibronectin-binding protein (Gfba) in pathogenicia		
RL	group G streptococci."		
RL	Infect. Immun. 64:2122-2129.(1996).		
DR	EMBL: U31115; AAB06623.1; -		
DR	INTERPRO: IPR001899; -		
DR	PROSITE: PS00345; GRAM_POS_ANCHORING; UNKNOWN.1.		
QZ	SEQUENCE 580 AA; 64975 MW; 69994BFA15C73A70 CRC64;		

Query Match	13.3%;	Score 523;	DB 2;	Length 580;
Best Local Similarity	24.8%;	Pred. No. 3.9e-23;		
Matches 180;	Conservative 106;	Mismatches 250;	Indels 190;	Gaps 23

0Y 20 SKNSRFLVTVGVGFLMFLALVTSVMCAKTYVGLGVSTSPALINPDSSSSRYRWYGVESVY 79
 23 TKRRKRFVAVTVGVGFMLLACAGATGEGQAVAADETVPRFKSPD--PDPWIGDAIT 80
 0Y 80 RGHPRVKKQFRAVHDLRVNLGSGRSQYVCFNLAKKAPFLGSDSSYKWKYKHKHDISTKFE 139
 Db 81 GAFLEK-----HDLNVLBESTPTQYVCFLVQNEPSSKVNQGFKKFFKKVYDGDMAVFKQ 134
 0Y 140 YAMSPRTGDELINQKLRVAVTNGHNPQNAANGIMEGLEPLNAIRVTOEAVVWYSDNAPISNP 139
 Db 135 YAANRVIDGDLERILNLVNIYNGYPSDANGIMKGLDRNALVYQTVAIWWYSDNSKFI-V 193
 0Y 200 DESFKREESNLVYTSQSLSMKQALKQIDNPNAIKTKPKQVDPDFOFSLSESEDKGQKYN 259
 Db 194 DEQMSKSLRDEISISQYKMLRDLRLKILSPDLKTYKNQDLPENYKILNLTSKD----- 247
 0Y 260 KGYQNLGSGLVPRKPPRGDPMPMPNPQPTSVLIRKAYAGISKLLEGATLQLTGDNV 319
 Db 248 NSIQMLLSTEVYQDNLQKRGEE-----270
 0Y 320 NSFQARVSSNDIGERIELSDGYTTLTELNSPAGYSIAEPITFEVAGKYVTTIDGKQIE 379
 Db 271 -----KEESPKEENKIPDLDG-HEIPVPEQPSDPVLPV-----IIDGEEVP 313
 0Y 360 NPNKATVPRYSVAVANDPEEFSYLTQNTAKFYAKKNGSSQVY----YCFNADLKSP 435
 Db 314 EYPSLESEFAPRLPRLPELDGQEV-----PEKPSIDLEIWPVRYEENKDDSP 361
 0Y 436 DSEDDGKTMTDEFTTGVEKY--THIAGRDLFKYTVKPRDTPDFTFLHKIKVIEKGYREK 494
 Db 362 AGE-----SGELEYITTEYVGNQ--QNPDIDK-----KLPNENG--SG 396
 0Y 495 QAIYESGLTETQLRAATQLAITYFTDSAEIDKRLKDYHGFQDNDSYLAVALIVEYAO 554
 Db 397 NMVETEDTKREPEVLMGQ-----SESVETKDTQGTGMSG-----430
 0Y 555 DSNPQLDLDLDFPIPNNNKYOSLGTQNHPRDLYDIIEMEKKEVIVYTNHLTKRTVTG 614
 Db 431 -QTPVQVETPTKBPQ-----VLMGQSSSEVFT-----KDTQTG 464
 0Y 615 IAGDRTQFHFETLKNKQELLSTQVTKDNTLFEKDGKATIMLKGESLTLQGLREGY 674
 Db 465 MSGQTP-----QVETEDTKRECVLMGQSSSEVGT-KDTQTGMS--GFSTAIYVEDTR 516
 0Y 675 SYLVKETDSEGYKAVNSQEVANAVTSKTYTSDETLAFENKKEPVVP-TGVDDKINGYL 733
 Db 517 PRLVHPFNNEKXEVENEKPT-----KNIPILPATGDIEVNLAF 558
 0Y 734 ALIVIA 739
 Db 559 GILLIS 564
 RESULT 6
 ID 033715 PRELIMINARY; PRT; 106 AA.
 AC 033715;
 DT 01-JAN-1998 (TREMBLrel, 05, Created)
 DT 01-JAN-1998 (TREMBLrel, 05, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel, 08, Last annotation update)
 DE FIBRONECTIN BINDING PROTEIN F (FRAGMENT).
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_taxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M STRAIN UMEA;
 RX MEDLINE=98129085; PubMed=9467904;
 RA Katerov V., Andreev A., Schalen C., Tocolian A.A.;
 RT "Protein F, a fibronectin-binding protein of Streptococcus pyogenes,
 also binds human fibrinogen: isolation of the protein and mapping of
 the binding region."

RA Katerov V., Andreev A., Schalen C., Totolian A.A.;
RT "Protein F", a fibronectin-binding protein of *Streptococcus pyogenes*,
RT also binds human fibrinogen: Isolation of the protein and mapping of
RT the binding region.";

Query Match	6.9%	Score 272.5;	DB 2;	Length 106;
Best Local Similarity	49.1%	Pred. No. 2e-09;		
Matches 53;	Conservative 17;	Mismatches 31;	Indels 7;	Gaps 2;
QY	51	FGLV-----ESTSTPAINPDSSSEKRWGCGSYNGCHPYKQFRVAHDLRVNLGSSRSYQ	105	
Db	1	FGQAVYASDEKTPVPEKSPD--PDIPMWGYAYAGGKGYGDISKTYHDLRVNLNGSQYQ	58	
QY	106	YVCENLKKAPFLGSDSYKKWYKKKHKGISTFKEFDYAMSPRITGDEL	153	
Db	59	YVCFNIOKIFPYNVKSVYQKWFKAEGNSDIFGFLAAMPVQGEELSQ	106	
RESULT 7				
ID	033714	PRELIMINARY;	PRT;	104 AA.
AC	033714;			
DT	01-JAN-1998 (TREMBLrel. 05, Created)			
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)			
DT	01-NOV-1998 (TREMBLrel. 08, Last annotation update)			
DE	FIBRONECTIN BINDING PROTEIN F (FRAGMENT).			
OS	Streptococcus pyogenes.			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;			
OC	Streptococcus.			
OX	NCBI_TaxID=1314;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-M4 STRAIN 281C;			
RX	MEDLINE=98129085; PubMed=9467904;			
RA	Katerov V., Andreev A., Schalen C., Tootlian A.A.;			
RT	"Protein F, a fibronectin-binding protein of Streptococcus pyogenes, also binds human fibrinogen: Isolation of the protein and mapping of the binding region."			
RT	Microbiology 144:119-126(1998).			
DR	EMBL; AF009913; AAC8160.1; -.			
FT	NON_TER	1		
FT	NON_TER	104		
FT	NON_TER	1		
SO	SEQUENCE	104 AA; 12055 MW; CF6C1A9E05A72850 CRC64;		
Query Match	6.7%	Score 262.5;	DB 2;	Length 104;
Best Local Similarity	48.1%	Pred. No. 7.5e-09;		
Matches 51;	Conservative 18;	Mismatches 30;	Indels 7;	Gaps 2;
QY	51	FGLV-----ESTSTPAINPDSSSEKRWGCGSYNGCHPYKQFRVAHDLRVNLGSSRSYQ	105	
Db	1	FGQAVYASDEKTPVPEKSPD--PDIPMWGYAYAGGKGYGDISKTYHDLRVNLNGSQYQ	58	
QY	106	YVCENLKKAPFLGSDSYKKWYKKKHKGISTFKEFDYAMSPRITGDEL	151	
Db	59	YVCFNIOKIFPYNVKSVYQKWFKAEGNSDIFGFLAAMPVQGEELSQ	104	
RESULT 8				
ID	033711	PRELIMINARY;	PRT;	108 AA.
AC	033711;			
DT	01-JAN-1998 (TREMBLrel. 05, Created)			
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)			
DT	01-NOV-1998 (TREMBLrel. 08, Last annotation update)			
DE	FIBRONECTIN BINDING PROTEIN F (FRAGMENT).			
OS	Streptococcus pyogenes.			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;			
OC	Streptococcus.			
OX	NCBI_TaxID=1314;			
RN	[1]			

[illegible]

DR 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE FIBRONECTIN BINDING PROTEIN F (FRAGMENT).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-M15 STRAIN 58/50;
RX MEDLINE=98129085; PubMed=9467904;
RA Katerov V., Andreev A., Schalen C., Totolian A.A.;
RT "Protein F, a fibronectin-binding protein of Streptococcus pyogenes,
also binds human fibrinogen: Isolation of the protein and mapping of
the binding region.";
RL Microbiology 144:119-126(1998).
DR EMBL: AF009917; AAC38164.1; -.
FT NON_TER 1 1
FT NON_TER 92 92
SQ SEQUENCE 92 AA; 10772 MW; 5C213D9CE669B82 CRC64;

Query Match 5.4%; Score 211.5; DB 2; Length 92;
Best Local Similarity 45.5%; Pred. No. 6.5e-06;
Matches 46; Conservative 15; Mismatches 25; Indels 15; Gaps 4;

OY 51 FGLV-----ESSTPNAINDSSEYRMWYGESYVRGHPYKQFRVA-HDLRVNLGSSRSY 104
DB 1 FGVAVAADEKTVPNKRN--SNPEFWGYDA-----YKGEAYHDLKVNLSKSKEX 51
OY 105 VYCFNLKKAFFPLGSDSVKWKYKKGISTKFEDYAMSPR 145
DB 52 QVYCFNLKRSFPRRTHSITNNFYKKIVGSGSVFKSYAENPR 92

RESULT 11
ID 033712 PRELIMINARY; PRT; 103 AA.
AC 033712;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE FIBRONECTIN BINDING PROTEIN F (FRAGMENT).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-M12 STRAIN 100085;
RX MEDLINE=98129085; PubMed=9467904;
RA Katerov V., Andreev A., Schalen C., Totolian A.A.;
RT "Protein F, a fibronectin-binding protein of Streptococcus pyogenes,
also binds human fibrinogen: Isolation of the protein and mapping of
the binding region.";
RL Microbiology 144:119-126(1998).
DR EMBL: AF009911; AAC38158.1; -.
FT NON_TER 1 1
FT NON_TER 103 103
SQ SEQUENCE 103 AA; 12011 MW; F056EBAC291A0477 CRC64;

Query Match 5.4%; Score 211.5; DB 2; Length 103;
Best Local Similarity 42.6%; Pred. No. 7.8e-06;
Matches 46; Conservative 17; Mismatches 32; Indels 13; Gaps 4;

OY 51 FGLV-----ESSTPNAINDSSEYRMWYGESYVRGHPYKQFRVAHDLRVNLGSSRSY 105
DB 1 FGVAVAADEKTVPNKSPD--PDYPWGYNSX-RG-----IFARYHNHKLKVNLSKSKEX 52
OY 106 VYCFNLKKAFFPLGSDSVKWKYKKGISTKFEDYAMSPRITDELNO 153
DB 53 AVCFNLTJTFPRPYSTNNFYKKIDGSGSAFESYANPRVIDENLDR 100

RESULT 12
ID 033719 PRELIMINARY; PRT; 102 AA.
AC 033719;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE FIBRONECTIN BINDING PROTEIN F (FRAGMENT).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-M18 STRAIN M18/104;
RX MEDLINE=98129085; PubMed=9467904;
RA Katerov V., Andreev A., Schalen C., Totolian A.A.;
RT "Protein F, a fibronectin-binding protein of Streptococcus pyogenes,
also binds human fibrinogen: Isolation of the protein and mapping of
the binding region.";
RL Microbiology 144:119-126(1998).
DR EMBL: AF009918; AAC38165.1; -.
FT NON_TER 1 1
FT NON_TER 102 102
SQ SEQUENCE 102 AA; 11795 MW; 66CCF38D847255FC CRC64;

Query Match 5.3%; Score 210.5; DB 2; Length 102;
Best Local Similarity 42.7%; Pred. No. 8.8e-06;
Matches 47; Conservative 16; Mismatches 34; Indels 13; Gaps 4;

OY 51 FGLV-----ESSTPNAINDSSEYRMWYGESYVRGHPYKQFRVAHDLRVNLGSSRSY 105
DB 1 FGVAVAADEKTVPNPSP--NPEFWGYDAY-RG-----SFLRYHDLNVNLGSSRSY 52
OY 106 VYCFNLKKAFFPLGSDSVKWKYKKGISTKFEDYAMSPRITDELNO 155
DB 53 VYCFNLVROEPSKVNGLRKNNFKYDGNVAFKRYAANPRVIDGLEINI 102

RESULT 13
ID 033716 PRELIMINARY; PRT; 102 AA.
AC 033716;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE FIBRONECTIN BINDING PROTEIN F (FRAGMENT).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-M12 STRAIN 73195/2110;
RX MEDLINE=98129085; PubMed=9467904;
RA Katerov V., Andreev A., Schalen C., Totolian A.A.;
RT "Protein F, a fibronectin-binding protein of Streptococcus pyogenes,
also binds human fibrinogen: Isolation of the protein and mapping of
the binding region.";
RL Microbiology 144:119-126(1998).
DR EMBL: AF009915; AAC38162.1; -.
FT NON_TER 1 1
FT NON_TER 102 102
SQ SEQUENCE 102 AA; 11932 MW; F6F935A2089DPCFD CRC64;

Query Match 5.3%; Score 209.5; DB 2; Length 102;
Best Local Similarity 42.6%; Pred. No. 1e-05;
Matches 46; Conservative 17; Mismatches 32; Indels 13; Gaps 4;

OY 51 FGLV-----ESSTPNAINDSSEYRMWYGESYVRGHPYKQFRVAHDLRVNLGSSRSY 105

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Db      1 FGOVAYAADEKTYVNFSPD--PDYPMWGYYSY-RG-----IFARYNLKNLKGSKKEYQ 52
QY      106 VYCFNLKKAFFPLGSDSSVKWKYKKHKGISTKFEDYAMSPRTGDELNQ 153
Db      53 AYCENLTKRYPPTPTSTNNFYKKIDGSGSAFKSYTANPRVLDENLDK 100

RESULT 14
ID      033713      PRELIMINARY;      PRT;      93 AA.
AC      033713;
DT      01-JAN-1998 (TREMblrel. 05, Created)
DT      01-JAN-1998 (TREMblrel. 05, last sequence update)
DT      01-NOV-1998 (TREMblrel. 08, last annotation update)
DE      FIBRONECTIN BINDING PROTEIN F (FRAGMENT).
OS      Streptococcus pyogenes.
OC      Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OX      Streptococcus.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-T27 STRAIN SF40;
RX      MEDLINE-98129085; PubMed-9467904;
RA      Katerov V., Andreev A., Schalen C., Totolian A.A.;
RT      "Protein F, a fibronectin-binding protein of Streptococcus pyogenes,
      also binds human fibrinogen: Isolation of the protein and mapping of
      the binding region.";
RL      Microbiology 144:119-126(1998).
DR      EMBL: AF009912; AAC38159.1; -.
FT      NON_TER      1      93
SQ      SEQUENCE      93 AA; 10742 MW; C51A35C75ABB85A8 CRC64;

Query Match
Best Local Similarity 5.2%; Score 205.5; DB 2; Length 93;
Matches 45; Conservative 16; Mismatches 27; Indels 13; Gaps 4;

QY      51 FGLV-----ESSTPNAINPDSSSEYRWYGYESYRGHPYRKQFRVAHDLRYNLEGSRSYQ 105
Db      1 FGOVAYAADEKTYVNFHSSP--NPEFPMYGYDSY-RG-----IFARYNLKNLKGSKKEYQ 52

QY      106 VYCFNLKKAFFPLGSDSSVKWKYKKHKGISTKFEDYAMSPRI 146
Db      53 AYCENLTKRYPPTPTSTNNFYKKIDGSGSAFKSYANPRV 93

RESULT 15
ID      033720      PRELIMINARY;      PRT;      102 AA.
AC      033720;
DT      01-JAN-1998 (TREMblrel. 05, Created)
DT      01-JAN-1998 (TREMblrel. 05, last sequence update)
DT      01-NOV-1998 (TREMblrel. 08, last annotation update)
DE      FIBRONECTIN BINDING PROTEIN F (FRAGMENT).
OS      Streptococcus pyogenes.
OC      Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OX      Streptococcus.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-M48 STRAINB4C3/48/1;
RX      MEDLINE-98129085; PubMed-9467904;
RA      Katerov V., Andreev A., Schalen C., Totolian A.A.;
RT      "Protein F, a fibronectin-binding protein of Streptococcus pyogenes,
      also binds human fibrinogen: Isolation of the protein and mapping of
      the binding region.";
RL      Microbiology 144:119-126(1998).
DR      EMBL: AF009919; AAC38166.1; -.
FT      NON_TER      1      102
SQ      SEQUENCE      102 AA; 11914 MW; AECDF38D82AE3EC7 CRC64;

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Query Match
Best Local Similarity 5.2%; Score 204.5; DB 2; Length 102;
Matches 46; Conservative 16; Mismatches 35; Indels 13; Gaps 4;

QY      51 FGLV-----ESSTPNAINPDSSSEYRWYGYESYRGHPYRKQFRVAHDLRYNLEGSRSYQ 105
Db      1 FGOVAYAADEKTYVNFYSSP--NPEFPMYGYDAY-RG-----WFLRYHDLNRYNLEGSASAYQ 52

QY      106 VYCFNLKKAFFPLGSDSSVKWKYKKHKGISTKFEDYAMSPRTGDELNQKL 155
Db      53 VYCFNLVROEPSKYNGLRKNMFKKVDGHNAYFKKYVANPRVLDGDLERNI 102

Search completed: June 7, 2001, 00:19:09
Job time: 122 sec

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